

FIGURE 10

GAGCGAGGCCGGGACTGAAGGTGTGGGTGTCTGAGCCCTCTGGCAGAGGGTTAAACCTGGGTG
AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCGCGGCACGTCGCGAGGACTTTGA
AGTCTTGAGCGCTCAAGTTTGTCCGTAGGTGAGAGAAGGCCATGAGAGGTGCCGCCACCGGC
ACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCCCGAGTCTTTGCTGCCGAAGCTG
TGACTGCGGATTGGAAGTCTTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCACAGAGCCC
TATTACCGGAATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG
AATTTCAAAGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGG
TGTATGGGGGAATACAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA
GAAATTTATCATAACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTT
CATTCTGTTATGGCTGGCGCTGGGGTTGGAGAAGTGCAGTGTTTGTGACTATATTCAACACAG
TGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAAATTGCAGGA
GCTGTACGGGAAGTCTTTTATGAGATAAACCTAGGCCTGCGTGGCCTGGTGGCTGGTGCCAT
AATTGGAGCCTTGTCTGGGCACTCCTGTAGGAGGCCTGCTGATGGCATTTTCAGAAGTACGCTG
GTGAGACTGTTTCAAGAAAGAAAAAGAGGATCGAAAGGCCTCCATGAGCTAAAACTGGAA
GAGTGGAAAGGCAGACTACAAGTTACTGAGCACCTCCTGAGAAAATTGAAAGTAGTTTACG
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTTCTAGAAAAC
CTTCAGTAATAGATAAAACAAGACAAGGACTGAAAGTGTCTGAACTTGAACTCACTGGAGA
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGC
TGACAAATTTAAGTGTGTTACCTGTGGTGGCAGTGGCTTGCTCTTGCTTTTTCTTTCTT
TTTAACTAAGAATGGGGCTGTGTACTCTCACTTTACTTATCCTTAAATTTAAATACATACT
TATGTTTGATTAAATCTATCAATATATGCATACATGGATATATCCACCACCTAGATTTTAA
GCAGTAAATAAAACATTTGCAAAAAGATTAAAGTTGAATTTTACAGTTT

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FIGURE 11

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32190, pI: 9.03, NX(S/T): 2
MEVPPPPAPRSFLCRALCLFPRVFAAEA VTADSEVLEERQKRLPYVPEPYYPESGWDRLRELF
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQA E IYHNRFD AVQSAH
RAATRGFIRYGWRGWRTAVFVTIFNTVNTSLNVYRNKDALSHFVIAGAVTGS LFRINVGLR
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELKLEEWKGRLQVTEHLPE
KIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD

Important Features:

Signal Peptide:

amino acids 1-24

Transmembrane domains:

amino acids 76-96 and 171-195

N-glycosylation site:

amino acids 153-156

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FIGURE 12

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAA
TACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT
AACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTTCGTTTCATG
GCTGGGCGCCGAACC

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA